

25
SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Lobb, Roy R.; Burkly, Linda C.
- (ii) TITLE OF INVENTION: Treatment for Asthma
- 10 (iii) NUMBER OF SEQUENCES: 11
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: LAHIVE & COCKFIELD
- (B) STREET: 60 State Street, Suite 510
- (C) CITY: Boston
- 15 (D) STATE: Massachusetts
- (E) COUNTRY: USA
- (F) ZIP: 02109-1875
- (v) COMPUTER READABLE FORM:
- 20 (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- 25 (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (vii) PRIOR APPLICATION DATA:
- 30 (A) APPLICATION NUMBER: US 08/374,331
- (B) FILING DATE: 18-JAN-1995
- (vii) PRIOR APPLICATION DATA:
- 35 (A) APPLICATION NUMBER: US 08/256,631
- (B) FILING DATE: 12-JUL-1994
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: PCT/US93/00030
- (B) FILING DATE: 12-JAN-1993
- 40 (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: US 07/821,768
- (B) FILING DATE: 13-JAN 1992
- 45 (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Myers, Louis (PLM)
- (B) REGISTRATION NUMBER: 35,965
- (C) REFERENCE/DOCKET NUMBER: BGP-021USCP2
- 50 (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: (617)227-7400
- (B) TELEFAX: (617)227-5941

55 (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 360 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

10 (B) LOCATION: 1..360

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1

15 (D) OTHER INFORMATION: /note= "pBAG159 insert: HP1/2 heavy
 chain variable region; amino acid 1 is Glu (E) but
 Gln (Q) may be substituted"

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTC	AAA	CTG	CAG	CAG	TCT	GGG	GCA	GAG	CTT	GTG	AAG	CCA	GGG	GCC	TCA	48
Val	Lys	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Lys	Pro	Gly	Ala	Ser	
1				5					10					15		

GTC	AAG	TTG	TCC	TGC	ACA	GCT	TCT	GGC	TTC	AAC	ATT	AAA	GAC	ACC	TAT	96
Val	Lys	Leu	Ser	Cys	Thr	Ala	Ser	Gly	Phe	Asn	Ile	Lys	Asp	Thr	Tyr	
			20					25					30			

ATG	CAC	TGG	GTG	AAG	CAG	AGG	CCT	GAA	CAG	GGC	CTG	GAG	TGG	ATT	GGA	144
Met	His	Trp	Val	Lys	Gln	Arg	Pro	Glu	Gln	Gly	Leu	Glu	Trp	Ile	Gly	
		35				40					45					

AGG	ATT	GAT	CCT	GCG	AGT	GGC	GAT	ACT	AAA	TAT	GAC	CCG	AAG	TTC	CAG	192
Arg	Ile	Asp	Pro	Ala	Ser	Gly	Asp	Thr	Lys	Tyr	Asp	Pro	Lys	Phe	Gln	
	50					55					60					

GTC	AAG	GCC	ACT	ATT	ACA	GCG	GAC	ACG	TCC	TCC	AAC	ACA	GCC	TGG	CTG	240
Val	Lys	Ala	Thr	Ile	Thr	Ala	Asp	Thr	Ser	Ser	Asn	Thr	Ala	Trp	Leu	
40	65				70				75					80		

CAG	CTC	AGC	AGC	CTG	ACA	TCT	GAG	GAC	ACT	GCC	GTC	TAC	TAC	TGT	GCA	288
Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	
				85				90						95		

GAC	GGA	ATG	TGG	GTA	TCA	ACG	GGA	TAT	GCT	CTG	GAC	TTC	TGG	GGC	CAA	336
Asp	Gly	Met	Trp	Val	Ser	Thr	Gly	Tyr	Ala	Leu	Asp	Phe	Trp	Gly	Gln	
			100				105						110			

GGG	ACC	ACG	GTC	ACC	GTC	TCC	TCA									360
Gly	Thr	Thr	Val	Thr	Val	Ser	Ser									
			115			120										

55 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser
1 5 10 15
Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
20 25 30
Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
15 35 40 45
Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
50 55 60
Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu
20 65 70 75 80
Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95
Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
100 105 110
Gly Thr Thr Val Thr Val Ser Ser
30 115 120

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

45 (A) NAME/KEY: CDS
(B) LOCATION: 1..318
(D) OTHER INFORMATION: /note= "HP1/2 light chain variable
region"

(ix) FEATURE:

50 (A) NAME/KEY: misc_feature
(B) LOCATION: 1
(D) OTHER INFORMATION: /note= "pBAG172 insert: HP1/2 light
chain variable region"

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGT ATT GTG ATG ACC CAG ACT CCC AAA TTC CTG CTT GTT TCA GCA GGA

28

Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly
1 5 10 15

5 GAC AGG GTT ACC ATA ACC TGC AAG GCC AGT CAG AGT GTG ACT AAT GAT 96
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp
20 25 30

10 GTA GCT TGG TAC CAA CAG AAG CCA GGG CAG TCT CCT AAA CTG CTG ATA 144
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
35 40 45

TAT TAT GCA TCC AAT CGC TAC ACT GGA GTC CCT GAT CGC TTC ACT GGC 192
Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

15 AGT GGA TAT GGG ACG GAT TTC ACT TTC ACC ATC AGC ACT GTG CAG GCT 240
Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
65 70 75 80

20 GAA GAC CTG GCA GTT TAT TTC TGT CAG CAG GAT TAT AGC TCT CCG TAC 288
Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr
85 90 95

25 ACG TTC GGA GGG GGG ACC AAG CTG GAG ATC 318
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
100 105

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

40 Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp
20 25 30

45 Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
35 40 45

50 Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
65 70 75 80

55 Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile

2) INFORMATION FOR SEQ ID NO: 5:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

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(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1338

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(ix) FEATURE:

- (A) NAME/KEY: VCAM-1 gene segment
- (B) LOCATION: 1..219
- (D) OTHER INFORMATION: This portion of the sequence corresponds, in part, to Exons I, II and III nucleotide sequence of Cybulsky et al. Proc. Nat'l. Acad. Sci. USA 88: 7861(1991).

25

(ix) FEATURE:

- (A) NAME/KEY: Hinge region
- (B) LOCATION: 220..229
- (D) OTHER INFORMATION: This portion of the sequence corresponds, in part, to Fig. 12A in PCT/US92/02050 and represents the hinge region of Human IgG1 heavy chain constant region.

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(ix) FEATURE:

- (A) NAME/KEY: Heavy chain constant region 2
- (B) LOCATION: 230..338
- (D) OTHER INFORMATION: This portion of the sequence corresponds, in part, to Fig. 12A in PCT/US92/02050 and represents the heavy chain constant region 2 of Human IgG1 heavy chain constant region.

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(ix) FEATURE:

- (A) NAME/KEY: Heavy chain constant region 3
- (B) LOCATION: 339..446
- (D) OTHER INFORMATION: This portion of the sequence corresponds, in part, to Fig. 12A in PCT/US92/02050 and represents the heavy chain constant region 3 of Human IgG1 heavy chain constant region.

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50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

55

ATG CCT GGG AAG ATG GTC GTG ATC CTT GGA GCC TCA AAT ATA CTT TGG
 Met Pro Gly Lys Met Val Val Ile Leu Gly Ala Ser Asn Ile Leu Trp
 110 115 120 125

48

ATA ATG TTT GCA GCT TCT CAA GCT TTT AAA ATC GAG ACC ACC CCA GAA

96

	Ile	Met	Phe	Ala	Ala	Ser	Gln	Ala	Phe	Lys	Ile	Glu	Thr	Thr	Pro	Glu	
				130						135					140		
5	TCT	AGA	TAT	CTT	GCT	CAG	ATT	GGT	GAC	TCC	GTC	TCA	TTG	ACT	TGC	AGC	144
	Ser	Arg	Tyr	Leu	Ala	Gln	Ile	Gly	Asp	Ser	Val	Ser	Leu	Thr	Cys	Ser	
				145					150					155			
10	ACC	ACA	GGC	TGT	GAG	TCC	CCA	TTT	TTC	TCT	TGG	AGA	ACC	CAG	ATA	GAT	192
	Thr	Thr	Gly	Cys	Glu	Ser	Pro	Phe	Phe	Ser	Trp	Arg	Thr	Gln	Ile	Asp	
			160					165					170				
15	AGT	CCA	CTG	AAT	GGG	AAG	GTG	ACG	AAT	GAG	GGG	ACC	ACA	TCT	ACG	CTG	240
	Ser	Pro	Leu	Asn	Gly	Lys	Val	Thr	Asn	Glu	Gly	Thr	Thr	Ser	Thr	Leu	
			175				180					185					
20	ACA	ATG	AAT	CCT	GTT	AGT	TTT	GGG	AAC	GAA	CAC	TCT	TAC	CTG	TGC	ACA	288
	Thr	Met	Asn	Pro	Val	Ser	Phe	Gly	Asn	Glu	His	Ser	Tyr	Leu	Cys	Thr	
	190					195					200					205	
25	GCA	ACT	TGT	GAA	TCT	AGG	AAA	TTG	GAA	AAA	GGA	ATC	CAG	GTG	GAG	ATC	336
	Ala	Thr	Cys	Glu	Ser	Arg	Lys	Leu	Glu	Lys	Gly	Ile	Gln	Val	Glu	Ile	
				210						215					220		
30	TAC	TCT	TTT	CCT	AAG	GAT	CCA	GAG	ATT	CAT	TTG	AGT	GGC	CCT	CTG	GAG	384
	Tyr	Ser	Phe	Pro	Lys	Asp	Pro	Glu	Ile	His	Leu	Ser	Gly	Pro	Leu	Glu	
				225					230					235			
35	GCT	GGG	AAG	CCG	ATC	ACA	GTC	AAG	TGT	TCA	GTT	GCT	GAT	GTA	TAC	CCA	432
	Ala	Gly	Lys	Pro	Ile	Thr	Val	Lys	Cys	Ser	Val	Ala	Asp	Val	Tyr	Pro	
			240					245					250				
40	TTT	GAC	AGG	CTG	GAG	ATA	GAC	TTA	CTG	AAA	GGA	GAT	CAT	CTC	ATG	AAG	480
	Phe	Asp	Arg	Leu	Glu	Ile	Asp	Leu	Leu	Lys	Gly	Asp	His	Leu	Met	Lys	
		255					260					265					
45	AGT	CAG	GAA	TTT	CTG	GAG	GAT	GCA	GAC	AGG	AAG	TCC	CTG	GAA	ACC	AAG	528
	Ser	Gln	Glu	Phe	Leu	Glu	Asp	Ala	Asp	Arg	Lys	Ser	Leu	Glu	Thr	Lys	
						275					280					285	
50	AGT	TTG	GAA	GTA	ACC	TTT	ACT	CCT	GTC	ATT	GAG	GAT	ATT	GGA	AAA	GTT	576
	Ser	Leu	Glu	Val	Thr	Phe	Thr	Pro	Val	Ile	Glu	Asp	Ile	Gly	Lys	Val	
					290					295					300		
55	CTT	GTT	TGC	CGA	GCT	AAA	TTA	CAC	ATT	GAT	GAA	ATG	GAT	TCT	GTG	CCC	624
	Leu	Val	Cys	Arg	Ala	Lys	Leu	His	Ile	Asp	Glu	Met	Asp	Ser	Val	Pro	
				305					310					315			
60	ACA	GTA	AGG	CAG	GCT	GTA	AAA	GAA	TTG	CAA	GTC	GAC	AAA	ACT	CAC	ACA	672
	Thr	Val	Arg	Gln	Ala	Val	Lys	Glu	Leu	Gln	Val	Asp	Lys	Thr	His	Thr	
			320					325					330				
65	TGC	CCA	CCG	TGC	CCA	GCA	CCT	GAA	CTC	CTG	GGG	GGA	CCG	TCA	GTC	TTC	720
	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	
			335				340					345					
70	CTC	TTC	CCC	CCA	AAA	CCC	AAG	GAC	ACC	CTC	ATG	ATC	TCC	CGG	ACC	CCT	768
	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	
						355					360					365	

	GAG	GTC	ACA	TGC	GTG	GTG	GTG	GAC	GTG	AGC	CAC	GAA	GAC	CCT	GAG	GTC	816
	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	
					370					375					380		
5	AAG	TTC	AAC	TGG	TAC	GTG	GAC	GGC	GTG	GAG	GTG	CAT	AAT	GCC	AAG	ACA	864
	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	
				385					390					395			
10	AAG	CCG	CGG	GAG	GAG	CAG	TAC	AAC	AGC	ACG	TAC	CGG	GTG	GTC	AGC	GTC	912
	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	
			400					405					410				
15	CTC	ACC	GTC	CTG	CAC	CAG	GAC	TGG	CTG	AAT	GGC	AAG	GAG	TAC	AAG	TGC	960
	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	
		415					420					425					
20	AAG	GTC	TCC	AAC	AAA	GCC	CTC	CCA	GCC	CCC	ATC	GAG	AAA	ACC	ATC	TCC	1008
	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	
	430					435					440					445	
25	AAA	GCC	AAA	GGG	CAG	CCC	CGA	GAA	CCA	CAG	GTG	TAC	ACC	CTG	CCC	CCA	1056
	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	
				450						455					460		
30	TCC	CGG	GAT	GAG	CTG	ACC	AAG	AAC	CAG	GTC	AGC	CTG	ACC	TGC	CTG	GTC	1104
	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	
				465					470					475			
35	AAA	GGC	TTC	TAT	CCC	AGC	GAC	ATC	GCC	GTG	GAG	TGG	GAG	AGC	AAT	GGG	1152
	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	
			480				485					490					
40	CAG	CCG	GAG	AAC	AAC	TAC	AAG	ACC	ACG	CCT	CCC	GTG	CTG	GAC	TCC	GAC	1200
	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	
		495					500					505					
45	GGC	TCC	TTC	TTC	CTC	TAC	AGC	AAG	CTC	ACC	GTG	GAC	AAG	AGC	AGG	TGG	1248
	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	
	510				515						520					525	
50	CAG	CAG	GGG	AAC	GTC	TTC	TCA	TGC	TCC	GTG	ATG	CAT	GAG	GCT	CTG	CAC	1296
	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	
				530						535					540		
55	AAC	CAC	TAC	ACG	CAG	AAG	AGC	CTC	TCC	CTG	TCT	CCG	GGT	AAA			1338
	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys			
				545					550					555			
50	TGAGT	GCGG															1347

(2) INFORMATION FOR SEQ ID NO: 6:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 6..23

(D) OTHER INFORMATION: This corresponds to Kinase
Primer 370-31.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

TCGTC GAC AAA ACT CAC ACA TGC C
Asp Lys Thr His Thr Cys
1 5

24

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: This corresponds to Kinase
Primer 370-32.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GTAAATGAGT GCGGCGGCCG CCAA

24

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GCGGCCGCGG TCCAACCACC AATCTCAAAG CTTGGTACCC GGAATTCAG ATCTGCAGCA 60
TGCTCGAGCT CTAGATATCG ATTCCATGGA TCCTCACATC CCAATCCGCG GCCGC 115

5

(2) INFORMATION FOR SEQ ID NO: 9:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 21..41

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

25 GAGCTCGAGG CGGCCGCACC ATG CCT GGG AAG ATG GTC GTG 41
Met Pro Gly Lys Met Val Val
1 5

30

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

45 AAGTCGACTT GCAATTCTTT TAC 23

(2) INFORMATION FOR SEQ ID NO: 11:

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TCGACGCGGC CGCG

5

CGCGTCGACGCGGC